



# FAX

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DATE: 5-7-01

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TO: Thomas Kowalski  
(ATTORNEY, AGENT, FIRM OR AGENCY)

674521-2001

(ATTORNEY'S DOCKET NUMBER OR APPLICATION NUMBER)

1-212-588-0500

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FROM: GERALD G. LEFFERS JR., EXAMINER, ART UNIT 1636

PHONE NUMBER (703) 308-6232

GROUP FAX NUMBER (703) 305-7213

REMARKS:

*Mr. Kowalski, here's the relevant pages of the most recent STIC CRF Error Report.*

*Thank you for agreeing to deal with this quickly,  
Gerry Leffers*

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745 FIFTH AVENUE NEW YORK, NEW YORK 10151

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May 07, 2001

VIA FEDERAL EXPRESS

Dale White  
Autopat, Inc.  
2001 Jefferson Davis Highway  
Lobby Level  
Arlington, VA 22202

Re: U.S. Patent Application Serial No. 09/430,590  
For: "AN UNUSUAL RETROTRANSPONSON FROM THE  
YEAST CANDIDA ALBICANS"  
FLH Ref. No. 674521-2001.1

Dear Dale:

We are enclosing the following documents:

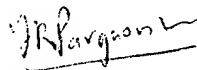
- 1) Sequence Listing (CRF and paper);
- 2) Response; and
- 3) Return receipt postcard.

Please expedite the processing of these papers by hand carrying them to Examiner G. Leffers Jr. (Group Art Unit 1636, Telephone No. (703) 308-6233) on **Tuesday, May 08, 2000.**

Kindly confirm by return facsimile that the papers have indeed been handed directly to Examiner G. Leffers Jr. Please also obtain acknowledgement of receipt on the enclosed postcard and return the postcard to us (by both facsimile and mail).

Please let us know if you have any questions.

Very truly yours,

  
Yateen Pargaonkar  
Legal Assistant to Thomas J. Kowalski

Enclosure

RECEIVED  
MAY 10 2001  
UNIT - 10151

**RAW SEQUENCE LISTING  
ERROR REPORT**BIOLOGY  
SYSTEMS  
BRANCH

APR 9 7 2001

RECEIVED

MAY -7 4:31

FROM: LAWRENCE  
FROM: H. H. H.

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/430,590 DSource: 1636Date Processed by STIC: 4-17-01

#18

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

 SERIAL NUMBER: 09/430,590D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

09/430, 5-90 L

p.6

&lt;210&gt; 147

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 147

gatacaaaat gcattaacgg cag

23

&lt;210&gt; 148

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 148

ctgccgttaa tgcattttgt atc

23

&lt;210&gt; 149

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 149

cgacggctgc agtttttcaa tgatgatttc aac

33

&lt;210&gt; 150

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 150

cgacggctgc agccttcaca ttataattg gc

32

Incomplete response for  
<213> as per section 1.823(b)  
of new sequence rules. See #11  
on the Error Summary Sheet.

Note: see also sequence  
#s 151, 152, 153, 154,  
155, 156.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.